

**Amendments to the Specification:**

Please amend the paragraphs at page 6, line 17 to page 7, line 10, as follows:

**-- BRIEF DESCRIPTION OF THE DRAWINGS**

FIG. 1A illustrates sequence alignments for the bacterial RNAP homologous RNA-exit-channel amino-acid sequences within rpoB ( $\beta$ ) (SEQ ID NOs:1-23), from *Escherichia coli* (SEQ ID NO:1); and corresponding residues of *Haemophilus influenzae* (SEQ ID NO:2), *Vibrio cholerae* (SEQ ID NO:3), *Pseudomonas aeruginosa* (SEQ ID NO:4), *Treponema pallidum* (SEQ ID NO:5), *Borrelia burgdorferi* (SEQ ID NO:6), *Xyella fastidiosa* (SEQ ID NO:7), *Camploacter jejuni* (SEQ ID NO:8), *Neisseria meningitides* (SEQ ID NO:9), *Rickettsia prowazekii* (SEQ ID NO:10), *Chlamydia trachomatis* (SEQ ID NO:11), *Mycoplasma pneumoniae* (SEQ ID NO:12), *Bacillus subtilis* (SEQ ID NO:13), *Staphylococcus aureus* (SEQ ID NO:14), *Mycobacterium tuberculosis* (SEQ ID NO:15), *Synechocystis* sp. (SEQ ID NO:16), *Aquifex aeolicus* (SEQ ID NO:17), *Deinococcus radiodurans* (SEQ ID NO:18), *Thermus thermophilus* (SEQ ID NO:19), and *Thermus aquaticus* (SEQ ID NO:20); and corresponding residues of the largest subunits of human RNAP I (SEQ ID NO:21), human RNAP II (SEQ ID NO:22), and human RNAP III (SEQ ID NO:23).

FIG. 1B illustrates sequence alignments for the bacterial RNAP homologous RNA-exit-channel amino-acid sequences within rpoC ( $\beta'$ ) (SEQ ID NOs: 24-69) from *Escherichia coli* (SEQ ID NOs: 24 and 25); and corresponding residues of *Haemophilus influenzae* (SEQ ID NOs: 26 and 27), *Vibrio cholerae* (SEQ ID NOs: 28 and 29), *Pseudomonas aeruginosa* (SEQ ID NOs: 30 and 31), *Treponema pallidum* (SEQ ID NOs: 32 and 33), *Borrelia burgdorferi* (SEQ ID NOs: 34 and 35), *Xyella fastidiosa* (SEQ ID NOs: 36 and 37), *Camploacter jejuni* (SEQ ID NOs: 38 and 39), *Neisseria meningitides* (SEQ ID NOs: 40 and 41), *Rickettsia prowazekii* (SEQ ID NOs: 42 and 43), *Chlamydia trachomatis* (SEQ ID NOs: 44 and 45), *Mycoplasma pneumoniae*

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(SEQ ID NOs: 46 and 47), *Bacillus subtilis* (SEQ ID NOs: 48 and 49), *Staphylococcus aureus* (SEQ ID NOs: 50 and 51), *Mycobacterium tuberculosis* (SEQ ID NOs: 52 and 53), *Synechocystis* sp. (SEQ ID NOs: 54 and 55), *Aquifex aeolicus* (SEQ ID NOs: 56 and 57), *Deinococcus radiodurans* (SEQ ID NOs: 58 and 59), *Thermus thermophilus* (SEQ ID NOs: 60 and 61), and *Thermus aquaticus* (SEQ ID NOs: 62 and 63); and corresponding residues of the largest subunits of human RNAP I (SEQ ID NOs: 64 and 65), human RNAP II (SEQ ID NOs: 66 and 67), and human RNAP III (SEQ ID NOs: 68 and 69).--